MICROBIOLOGIE, INFECTIOLOGIE ET IMMUNOLOGIE

Université de Montréal

CONFÉRENCE

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Characterizing microbial interaction mechanisms in microbial communities

Microbial communities, also known as microbiomes, are ubiquitous and contribute to essential function to sustain life on Earth. Microbial community structure and function rely on complex interactions whose underlying molecular mechanisms are poorly understood. Model microbiomes such as cheese rinds are simple microbial communities that represent a good opportunity to broadly investigate these mechanisms. Combining an experimental cheese rind community and genomic approach, I initially developed a strategy to decipher interaction mechanisms in microbiomes and further investigate their organization. Briefly, I introduced *E. coli* into a simple cheese rind community and identified the differences in *E. coli*'s genetic requirements for growth with the community and requirements for growth alone using Random Barcode Transposon Sequencing (RB-TnSeq) and RNASeq. Variation of genetic requirements between interactive and non-interactive conditions as well as the variation of gene expression are used to infer interaction mechanisms. Using the same approach to identify interactions between *E. coli* and single community members in pairwise cultures, I mapped whether interactions in the community were simple pairwise interactions or higher order interactions. Our analysis identifies a variety of interaction mechanisms within the community, including amino acid cross-feeding, toxic stress and metabolic competition; that result from a combination of pairwise and higher-order interactions. Quantitative and modeling approaches are now being used to further decipher the intricacy of these higher order interactions.

Overall, this work provides a framework for using genomic approaches and the model organism *E. coli* as a readout to investigate microbial interactions in microbial communities.

Thursday January 30th, 2020 at 11h30
Pavillon Claire-McNicoll, Room Z-205

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